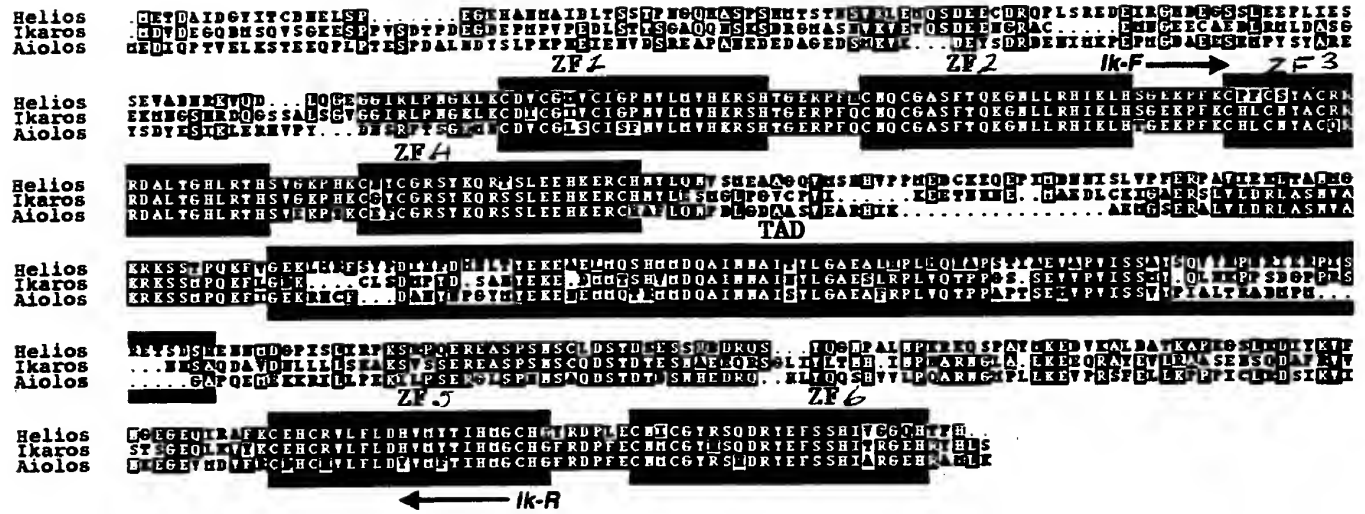


FIG. 1

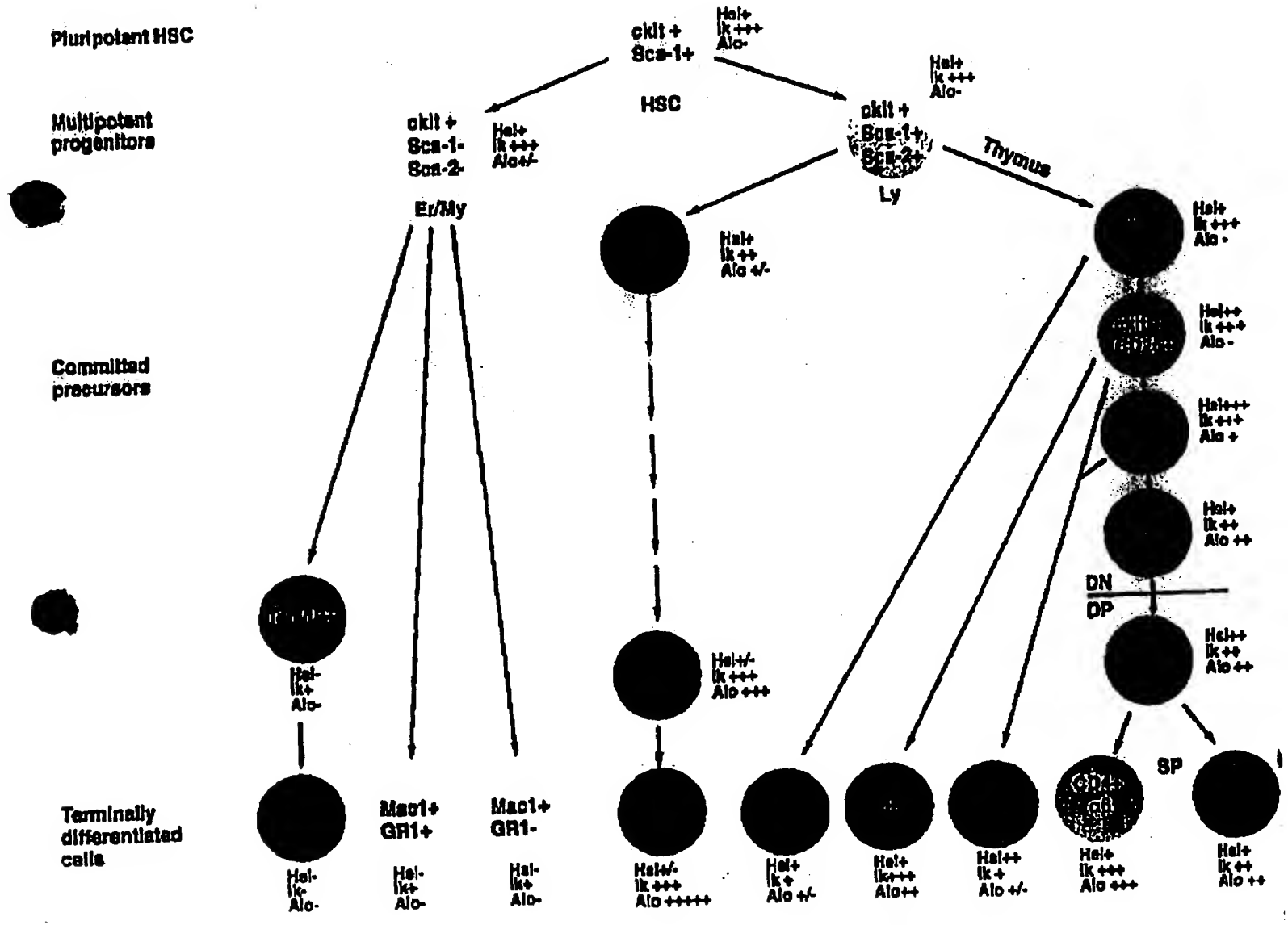

Pluripotent HSC
Multipotent progenitors
Committed precursors
Terminally differentiated cells
ckit +
Sca-1+
HSC
Hsl+
Ik +++
Alo-
ckit +
Sca-1-
Sca-2-
Er/My
Hsl+
Ik +++
Alo+/-
ckit +
Sca-1+
Sca-2+
Ly
Thymus
Hsl+
Ik ++
Alo +/-
Hsl+
Ik +++
Alo -
Hsl++
Ik +++
Alo -
Hsl+++
Ik +++
Alo +
Hsl+
Ik ++
Alo ++
DN
DP
Hsl++
Ik ++
Alo ++
SP
Hsl-
Ik+
Alo-
Hsl-
Ik-
Alo-
Mac1+
GR1+
Hsl-
Ik+
Alo-
Mac1+
GR1-
Hsl-
Ik+
Alo-
Hsl+/-
Ik +++
Alo +++
Hsl+/-
Ik +++
Alo +++++
Hsl+
Ik +
Alo +/-
Hsl+
Ik+++
Alo++
Hsl++
Ik +
Alo +/-
Hsl+
Ik +++
Alo +++
Hsl+
Ik ++
Alo ++

FIG. 2

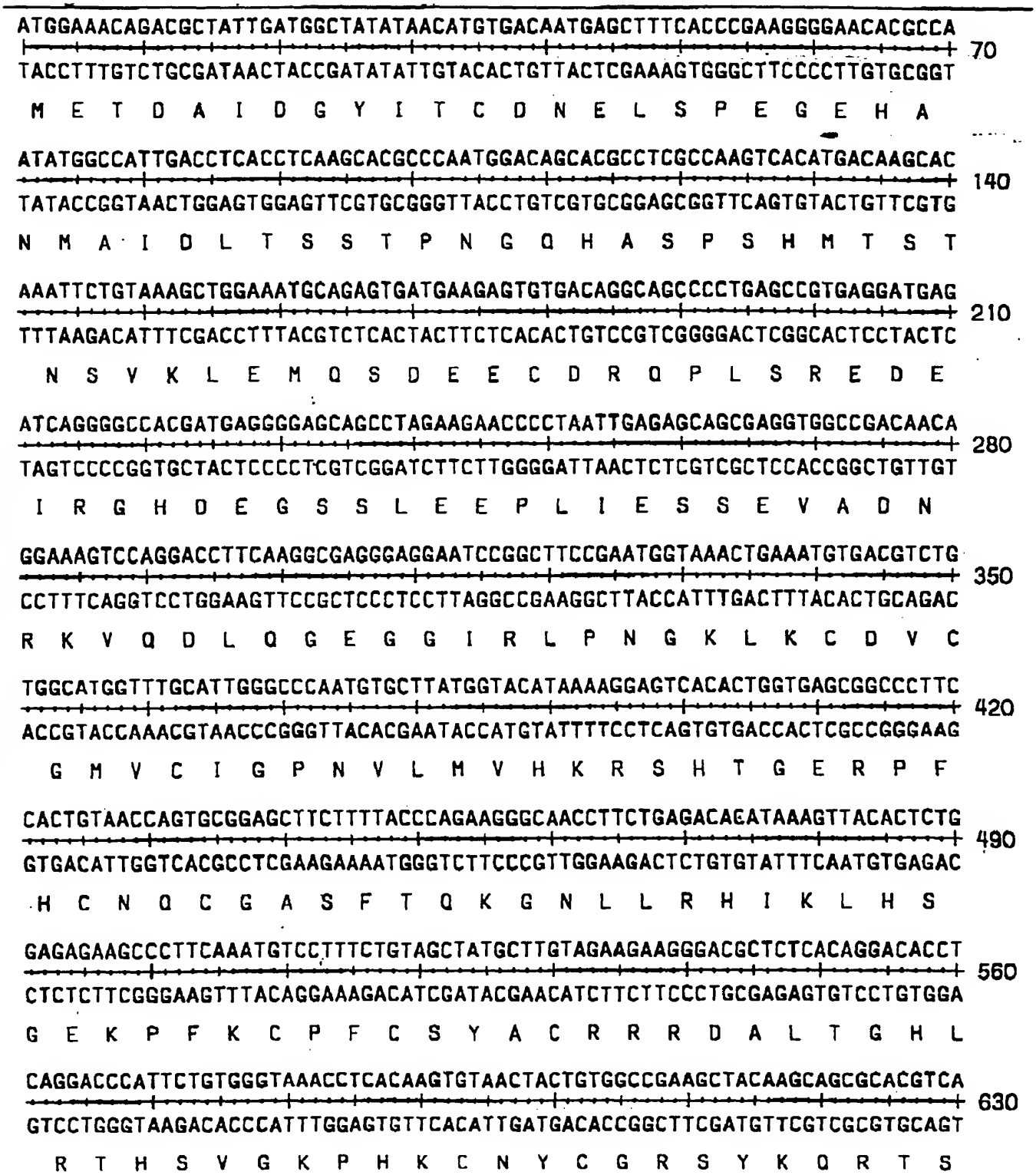
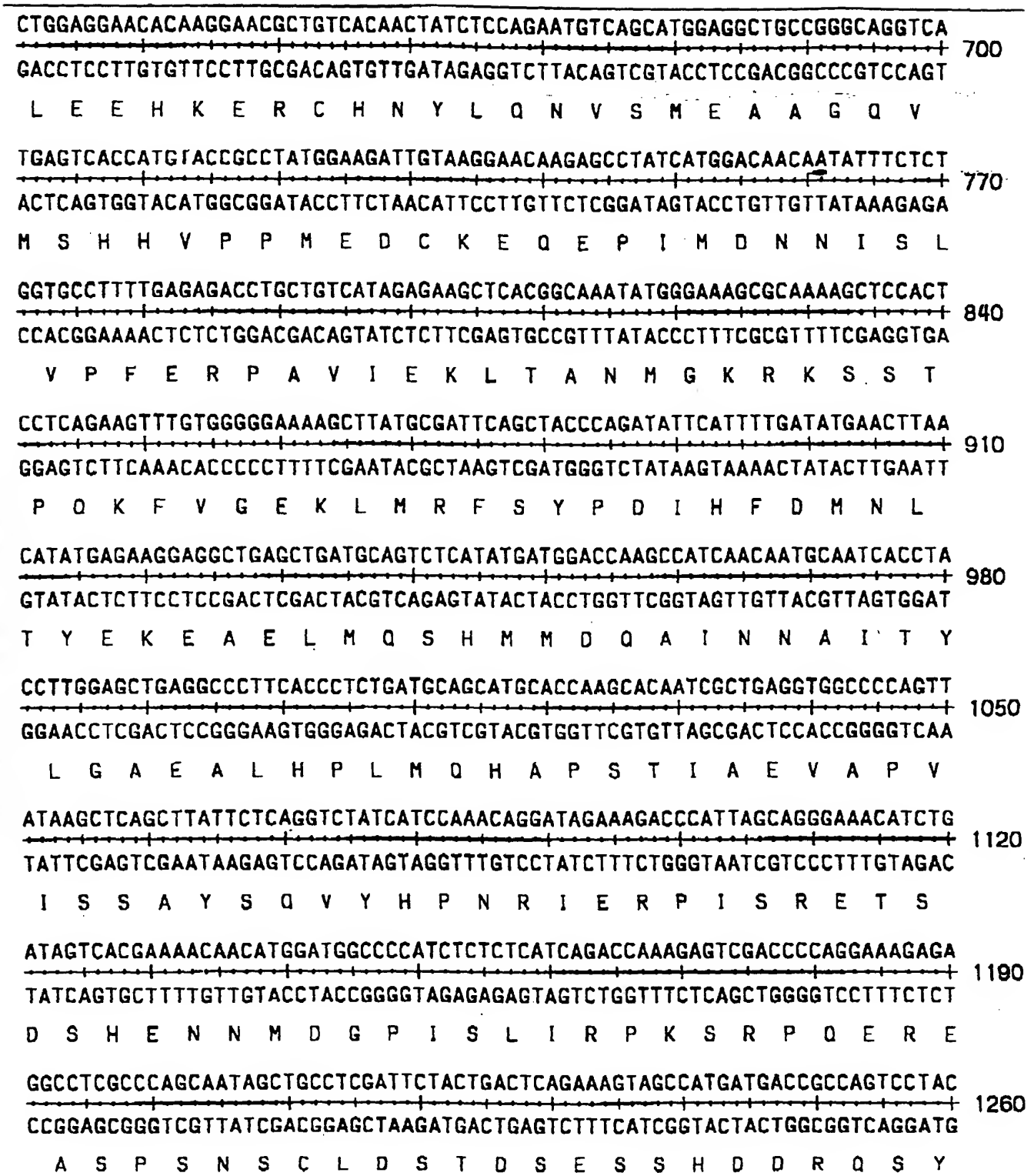

ATGGAAACAGACGCTATTGATGGCTATATAACATGTGACAATGAGCTTTCACCCGAAGGGGAACACGCCA
70
TACCTTTGTCTGCGATAACTACCGATATATTGTACACTGTTACTCGAAAGTGGGCTTCCCCTTGTGCGGT
M E T D A I D G Y I T C D N E L S P E G E H A
ATATGGCCATTGACCTCACCTCAAGCACGCCCAATGGACAGCACGCCTCGCCAAGTCACATGACAAGCAC
140
TATACCGGTAACTGGAGTGGAGTTCGTGCGGGTTACCTGTCGTGCGGAGCGGTTCAGTGTACTGTTCGTG
N M A I D L T S S T P N G Q H A S P S H M T S T
AAATTCTGTAAAGCTGGAAATGCAGAGTGATGAAGAGTGTGACAGGCAGCCCCTGAGCCGTGAGGATGAG
210
TTTAAGACATTTCGACCTTTACGTCTCACTACTTCTCACACTGTCCGTCGGGGACTCGGCACTCCTACTC
N S V K L E M Q S D E E C D R Q P L S R E D E
ATCAGGGGCCACGATGAGGGGAGCAGCCTAGAAGAACCCCTAATTGAGAGCAGCGAGGTGGCCGACAACA
280
TAGTCCCCGGTGCTACTCCCCTCGTCGGATCTTCTTGGGGATTAACTCTCGTCGCTCCACCGGCTGTTGT
I R G H D E G S S L E E P L I E S S E V A D N
GGAAAGTCCAGGACCTTCAAGGCGAGGGAGGAATCCGGCTTCCGAATGGTAAACTGAAATGTGACGTCTG
350
CCTTTCAGGTCCTGGAAGTTCCGCTCCCTCCTTAGGCCGAAGGCTTACCATTTGACTTTACACTGCAGAC
R K V Q D L Q G E G G I R L P N G K L K C D V C
TGGCATGGTTTGCATTGGGCCCAATGTGCTTATGGTACATAAAAGGAGTCACACTGGTGAGCGGCCCTTC
420
ACCGTACCAAACGTAACCCGGGTTACACGAATACCATGTATTTTCCTCAGTGTGACCACTCGCCGGGAAG
G M V C I G P N V L M V H K R S H T G E R P F
CACTGTAACCAGTGCGGAGCTTCTTTTACCCAGAAGGGCAACCTTCTGAGACACATAAAGTTACACTCTG
490
GTGACATTGGTCACGCCTCGAAGAAAATGGGTCTTCCCGTTGGAAGACTCTGTGTATTTCAATGTGAGAC
H C N Q C G A S F T Q K G N L L R H I K L H S
GAGAGAAGCCCTTCAAATGTCCTTTCTGTAGCTATGCTTGTAGAAGAAGGGACGCTCTCACAGGACACCT
560
CTCTCTTCGGGAAGTTTACAGGAAAGACATCGATACGAACATCTTCTTCCCTGCGAGAGTGTCCTGTGGA
G E K P F K C P F C S Y A C R R R D A L T G H L
CAGGACCCATTCTGTGGGTAAACCTCACAAGTGTAACTACTGTGGCCGAAGCTACAAGCAGCGCACGTCA
630
GTCCTGGGTAAGACACCCATTTGGAGTGTTCACATTGATGACACCGGCTTCGATGTTCGTCGCGTGCAGT
R T H S V G K P H K C N Y C G R S Y K Q R T S

FIG. 3
(1 of 3)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700
GACCTCCTTGTGTTCCTTGCGACAGTGTTGATAGAGGTCTTACAGTCGTACCTCCGACGGCCCGTCCAGT
L E E H K E R C H N Y L Q N V S M E A A G Q V
TGAGTCACCATGTACCGCCTATGGAAGATTGTAAGGAACAAGAGCCTATCATGGACAACAATATTTCTCT
770
ACTCAGTGGTACATGGCGGATACCTTCTAACATTCCTTGTTCTCGGATAGTACCTGTTGTTATAAAGAGA
M S H H V P P M E D C K E Q E P I M D N N I S L
GGTGCCTTTTGAGAGACCTGCTGTCATAGAGAAGCTCACGGCAAATATGGGAAAGCGCAAAAGCTCCACT
840
CCACGGAAAACTCTCTGGACGACAGTATCTCTTCGAGTGCCGTTTATACCCTTTCGCGTTTTCGAGGTGA
V P F E R P A V I E K L T A N M G K R K S S T
CCTCAGAAGTTTGTGGGGGAAAAGCTTATGCGATTCAGCTACCCAGATATTCATTTTGATATGAACTTAA
910
GGAGTCTTCAAACACCCCCTTTTCGAATACGCTAAGTCGATGGGTCTATAAGTAAAACTATACTTGAATT
P Q K F V G E K L M R F S Y P D I H F D M N L
CATATGAGAAGGAGGCTGAGCTGATGCAGTCTCATATGATGGACCAAGCCATCAACAATGCAATCACCTA
980
GTATACTCTTCCTCCGACTCGACTACGTCAGAGTATACTACCTGGTTCGGTAGTTGTTACGTTAGTGGAT
T Y E K E A E L M Q S H M M D Q A I N N A I T Y
CCTTGGAGCTGAGGCCCTTCACCCTCTGATGCAGCATGCACCAAGCACAATCGCTGAGGTGGCCCCAGTT
1050
GGAACCTCGACTCCGGGAAGTGGGAGACTACGTCGTACGTGGTTCGTGTTAGCGACTCCACCGGGGTCAA
L G A E A L H P L M Q H A P S T I A E V A P V
ATAAGCTCAGCTTATTCTCAGGTCTATCATCCAAACAGGATAGAAAGACCCATTAGCAGGGAAACATCTG
1120
TATTCGAGTCGAATAAGAGTCCAGATAGTAGGTTTGTCCTATCTTTCTGGGTAATCGTCCCTTTGTAGAC
I S S A Y S Q V Y H P N R I E R P I S R E T S
ATAGTCACGAAAACAACATGGATGGCCCCATCTCTCTCATCAGACCAAAGAGTCGACCCCAGGAAAGAGA
1190
TATCAGTGCTTTTGTTGTACCTACCGGGGTAGAGAGAGTAGTCTGGTTTCTCAGCTGGGGTCCTTTCTCT
D S H E N N M D G P I S L I R P K S R P Q E R E
GGCCTCGCCCAGCAATAGCTGCCTCGATTCTACTGACTCAGAAAGTAGCCATGATGACCGCCAGTCCTAC
1260
CCGGAGCGGGTCGTTATCGACGGAGCTAAGATGACTGAGTCTTTCATCGGTACTACTGGCGGTCAGGATG
A S P S N S C L D S T D S E S S H D D R Q S Y

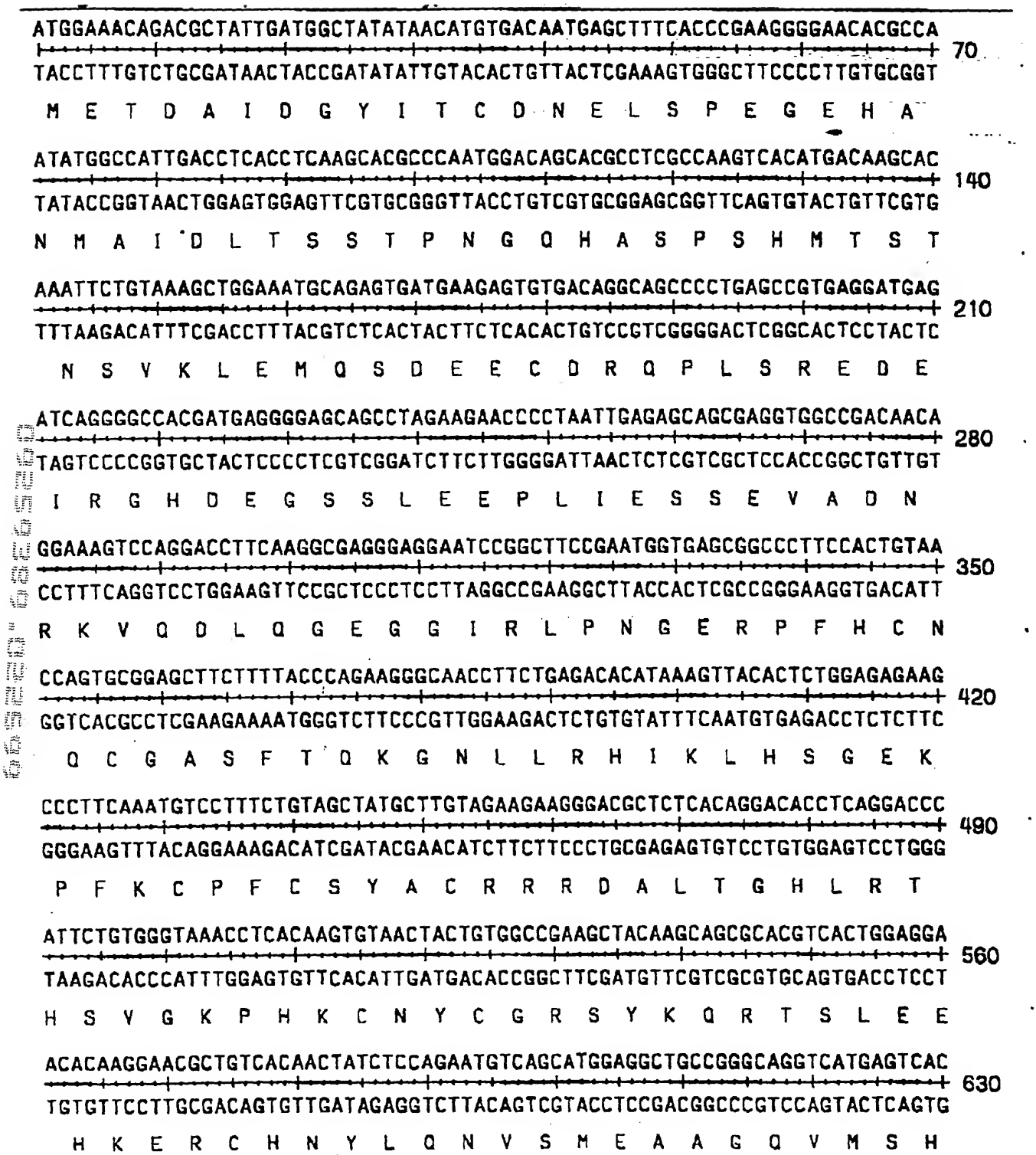
FIG. 3

(2 of 3)


CAAGGAAACCCTGCCTTAAATCCCAAGAGGAAACAAAGCCCAGCTTACATGAAGGAGGATGTCAAGGCTT
1330
GTTCCTTTGGGACGGAATTTAGGGTTCTCCTTTGTTTCGGGTCGAATGTACTTCCTCCTACAGTTCCGAA
Q G N P A L N P K R K Q S P A Y M K E D V K A
TGGATGCTACCAAGGCCCCCAAGGGCTCTCTGAAGGACATCTATAAGGTTTTCAATGGAGAAGGAGAACA
1400
ACCTACGATGGTTCCGGGGGTTCCCGAGAGACTTCCTGTAGATATTCCAAAAGTTACCTCTTCCTCTTGT
L D A T K A P K G S L K D I Y K V F N G E G E Q
GATAAGGGCCTTCAAGTGTGAGCACTGCCGAGTCCTTTTTCTAGACCATGTCATGTACACCATTCACATG
1470
CTATTCCCGGAAGTTCACACTCGTGACGGCTCAGGAAAAAGATCTGGTACAGTACATGTGGTAAGTGTAC
I R A F K C E H C R V L F L D H V M Y T I H M
GGTTGCCATGGCTACCGGGACCCACTGGAATGCAACATCTGTGGCTACAGAAGCCAGGACCGCTACGAAT
1540
CCAACGGTACCGATGGCCCTGGGTGACCTTACGTTGTAGACACCGATGTCTTCGGTCCTGGCGATGCTTA
G C H G Y R Q P L E C N I C G Y R S Q D R Y E
TTTCATCACACATTGTTGGGGGGCAGCACACATTCCACTAGGCGTTTGCATTCCAAGG
1598
AAAGTAGTGTGTAACAACCCCCCGTCGTGTGTAAGGTGATCCGCAAACGTAAGGTTCC
F S S H I V G G Q H T F H . A F A F Q G

FIG. 3

(3 of 3)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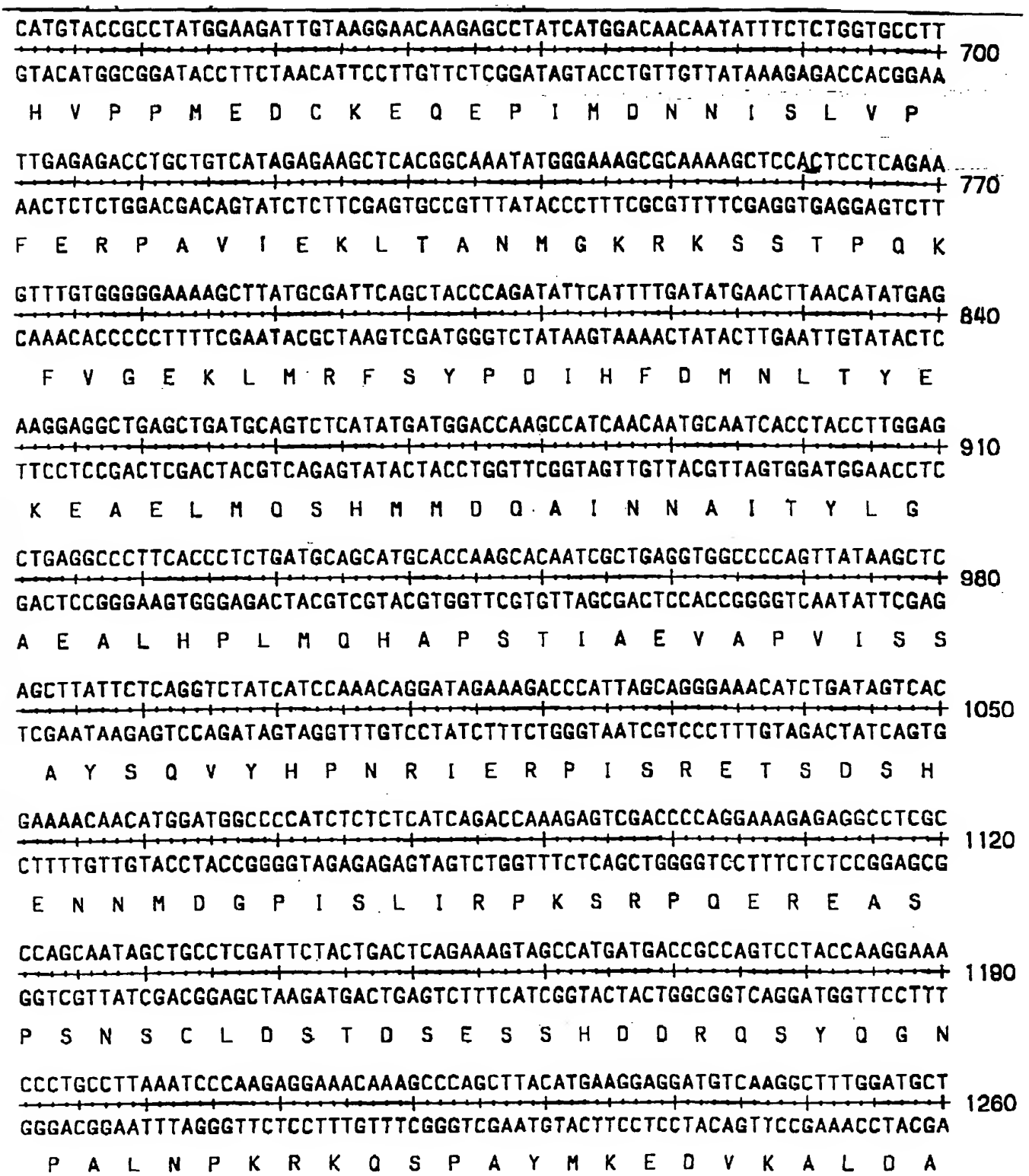
TACCTTTGTCTGCGATAACTACCGATATATTGTACACTGTTACTCGAAAGTGGGCTTCCCCTTGTGCGGT
M E T D A I D G Y I T C D N E L S P E G E H A
70
ATATGGCCATTGACCTCACCTCAAGCACGCCCAATGGACAGCACGCCTCGCCAAGTCACATGACAAGCAC
TATACCGGTAACTGGAGTGGAGTTCGTGCGGGTTACCTGTCGTGCGGAGCGGTTCAGTGTACTGTTCGTG
N M A I D L T S S T P N G Q H A S P S H M T S T
140
AAATTCTGTAAAGCTGGAAATGCAGAGTGATGAAGAGTGTGACAGGCAGCCCCTGAGCCGTGAGGATGAG
TTTAAGACATTTCGACCTTTACGTCTCACTACTTCTCACACTGTCCGTCGGGGACTCGGCACTCCTACTC
N S V K L E M Q S D E E C D R Q P L S R E D E
210
ATCAGGGGCCACGATGAGGGGAGCAGCCTAGAAGAACCCCTAATTGAGAGCAGCGAGGTGGCCGACAACA
TAGTCCCCGGTGCTACTCCCCTCGTCGGATCTTCTTGGGGATTAACTCTCGTCGCTCCACCGGCTGTTGT
I R G H D E G S S L E E P L I E S S E V A D N
280
GGAAAGTCCAGGACCTTCAAGGCGAGGGAGGAATCCGGCTTCCGAATGGTGAGCGGCCCTTCCACTGTAA
CCTTTCAGGTCCTGGAAGTTCCGCTCCCTCCTTAGGCCGAAGGCTTACCACTCGCCGGGAAGGTGACATT
R K V Q D L Q G E G G I R L P N G E R P F H C N
350
CCAGTGCGGAGCTTCTTTTACCCAGAAGGGCAACCTTCTGAGACACATAAAGTTACACTCTGGAGAGAAG
GGTCACGCCTCGAAGAAAATGGGTCTTCCCGTTGGAAGACTCTGTGTATTTCAATGTGAGACCTCTCTTC
Q C G A S F T Q K G N L L R H I K L H S G E K
420
CCCTTCAAATGTCCTTTCTGTAGCTATGCTTGTAGAAGAAGGGACGCTCTCACAGGACACCTCAGGACCC
GGGAAGTTTACAGGAAAGACATCGATACGAACATCTTCTTCCCTGCGAGAGTGTCCTGTGGAGTCCTGGG
P F K C P F C S Y A C R R R D A L T G H L R T
490
ATTCTGTGGGTAAACCTCACAAGTGTAACTACTGTGGCCGAAGCTACAAGCAGCGCACGTCACTGGAGGA
TAAGACACCCATTTGGAGTGTTCACATTGATGACACCGGCTTCGATGTTCGTCGCGTGCAGTGACCTCCT
H S V G K P H K C N Y C G R S Y K Q R T S L E E
560
ACACAAGGAACGCTGTCACAACTATCTCCAGAATGTCAGCATGGAGGCTGCCGGGCAGGTCATGAGTCAC
TGTGTTCCTTGCGACAGTGTTGATAGAGGTCTTACAGTCGTACCTCCGACGGCCCGTCCAGTACTCAGTG
H K E R C H N Y L Q N V S M E A A G Q V M S H
630

FIG. 4
(1 of 3)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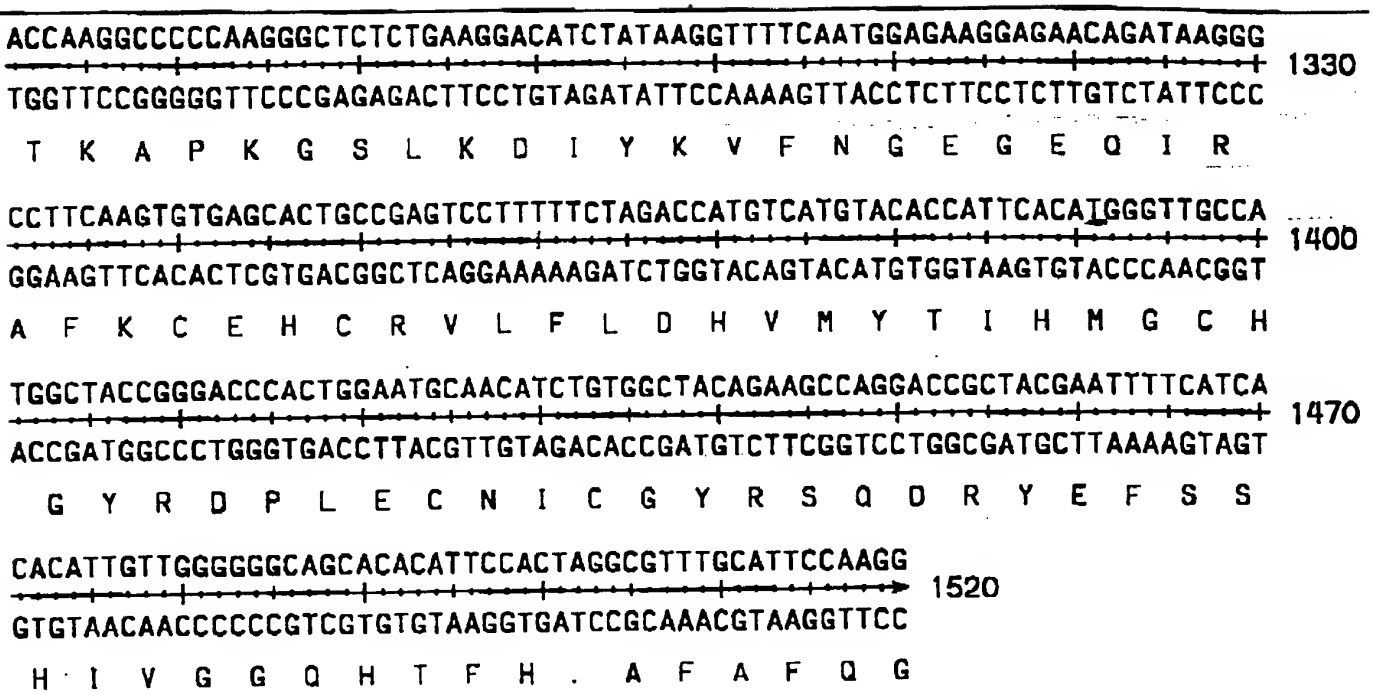
700
GTACATGGCGGATACCTTCTAACATTCCTTGTTCTCGGATAGTACCTGTTGTTATAAAGAGACCACGGAA
H V P P M E D C K E Q E P I M D N N I S L V P
TTGAGAGACCTGCTGTCATAGAGAAGCTCACGGCAAATATGGGAAAGCGCAAAAGCTCCACTCCTCAGAA
770
AACTCTCTGGACGACAGTATCTCTTCGAGTGCCGTTTATACCCTTTCGCGTTTTCGAGGTGAGGAGTCTT
F E R P A V I E K L T A N M G K R K S S T P Q K
GTTTGTGGGGGAAAAGCTTATGCGATTCAGCTACCCAGATATTCATTTTGATATGAACTTAACATATGAG
840
CAAACACCCCCTTTTCGAATACGCTAAGTCGATGGGTCTATAAGTAAAACTATACTTGAATTGTATACTC
F V G E K L M R F S Y P D I H F D M N L T Y E
AAGGAGGCTGAGCTGATGCAGTCTCATATGATGGACCAAGCCATCAACAATGCAATCACCTACCTTGGAG
910
TTCCTCCGACTCGACTACGTCAGAGTATACTACCTGGTTCGGTAGTTGTTACGTTAGTGGATGGAACCTC
K E A E L M Q S H M M D Q A I N N A I T Y L G
CTGAGGCCCTTCACCCTCTGATGCAGCATGCACCAAGCACAATCGCTGAGGTGGCCCCAGTTATAAGCTC
980
GACTCCGGGAAGTGGGAGACTACGTCGTACGTGGTTCGTGTTAGCGACTCCACCGGGGTCAATATTCGAG
A E A L H P L M Q H A P S T I A E V A P V I S S
AGCTTATTCTCAGGTCTATCATCCAAACAGGATAGAAAGACCCATTAGCAGGGAAACATCTGATAGTCAC
1050
TCGAATAAGAGTCCAGATAGTAGGTTTGTCCTATCTTTCTGGGTAATCGTCCCTTTGTAGACTATCAGTG
A Y S Q V Y H P N R I E R P I S R E T S D S H
GAAAACAACATGGATGGCCCCATCTCTCTCATCAGACCAAAGAGTCGACCCCAGGAAAGAGAGGCCTCGC
1120
CTTTTGTTGTACCTACCGGGGTAGAGAGAGTAGTCTGGTTTCTCAGCTGGGGTCCTTTCTCTCCGGAGCG
E N N M D G P I S L I R P K S R P Q E R E A S
CCAGCAATAGCTGCCTCGATTCTACTGACTCAGAAAGTAGCCATGATGACCGCCAGTCCTACCAAGGAAA
1190
GGTCGTTATCGACGGAGCTAAGATGACTGAGTCTTTCATCGGTACTACTGGCGGTCAGGATGGTTCCTTT
P S N S C L D S T D S E S S H D D R Q S Y Q G N
CCCTGCCTTAAATCCCAAGAGGAAACAAAGCCCAGCTTACATGAAGGAGGATGTCAAGGCTTTGGATGCT
1260
GGGACGGAATTTAGGGTTCTCCTTTGTTTCGGGTCGAATGTACTTCCTCCTACAGTTCCGAAACCTACGA
P A L N P K R K Q S P A Y M K E D V K A L D A

FIG. 4

(2 of 3)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1330
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T K A P K G S L K D I Y K V F N G E G E Q I R
CCTTCAAGTGTGAGCACTGCCGAGTCCTTTTTCTAGACCATGTCATGTACACCATTCACATGGGTTGCCA
1400
GGAAGTTCACACTCGTGACGGCTCAGGAAAAAGATCTGGTACAGTACATGTGGTAAGTGTACCCAACGGT
A F K C E H C R V L F L D H V M Y T I H M G C H
TGGCTACCGGGACCCACTGGAATGCAACATCTGTGGCTACAGAAGCCAGGACCGCTACGAATTTTCATCA
1470
ACCGATGGCCCTGGGTGACCTTACGTTGTAGACACCGATGTCTTCGGTCCTGGCGATGCTTAAAAGTAGT
G Y R D P L E C N I C G Y R S Q D R Y E F S S
CACATTGTTGGGGGGCAGCACACATTCCACTAGGCGTTTGCATTCCAAGG
1520
GTGTAACAACCCCCCGTCGTGTGTAAGGTGATCCGCAAACGTAAGGTTCC
H I V G G Q H T F H . A F A F Q G

FIG. 4

(3 of 3)

```
1/1                                                 31/11
GCC CGG GCA GGT CGC ATT GCT ATA GCA CTG ACT GAC CTC TCT CTC TCT CTT TTT TTT CCT
A   R   A   G   R   I   A   I   A   L   T   D   L   S   L   S   L   F   F   P
61/21                                               91/31
CTT TCC TGA AAC CCG ACA TTG TCA CCT CCT CTT TGA GGG TTA GAA GAA GCT GAG ATC TCC
L   S   *   N   P   T   L   S   P   P   L   *   G   L   E   E   A   E   I   S
121/41                                              151/51
CGA CAG AGC TGG AAA TGG TGA TGA ATC TTT TTT AAT CAA AGG ACA ATT TCT TTT CAT TGC
R   Q   S   W   K   W   *   *   I   F   F   N   Q   R   T   I   S   F   H   C
181/61                                              211/71
ACT TTG ACT ATG GAA ACA GAG GCT ATT GAT GGC TAT ATA ACG TGT GAC AAT GAG CTT TCA
T   L   T   M   E   T   E   A   I   D   G   Y   I   T   C   D   N   E   L   S
241/81                                              271/91
CCC GAA AGG GAG CAC TCC AAT ATG GCA ATT GAC CTC ACC TCA AGC ACA CCC AAT GGA CAG
P   E   R   E   H   S   N   M   A   I   D   L   T   S   S   T   P   N   G   Q
301/101                                             331/111
CAT GCC TCA CCA AGT CAC ATG ACA AGC ACA GAT TCA GTA AAG CTA GAA ATG CAG AGT GAT
H   A   S   P   S   H   M   T   S   T   D   S   V   K   L   E   M   Q   S   D
361/121                                             391/131
GAA GAG TGT GAC AGG AAA CCC CTG AGC CGT GAA GAT GAG ATC AGG GGC CAT GAT GAG GGT
E   E   C   D   R   K   P   L   S   R   E   D   E   I   R   G   H   D   E   G
421/141                                             451/151
AGC AGC CTA GAA GAA CCC CTA ATT GAG AGC AGC GAG GTG GCT GAC AAC AGG GAA GTC CAG
S   S   L   E   E   P   L   I   E   S   S   E   V   A   D   N   R   E   V   Q
481/161                                             511/171
GAG CTT CAA GGC GAG GGA GGA ATC CGG CTT CCG AAT GGT AAA CTG AAA TGT GAC GTC TGT
E   L   Q   G   E   G   G   I   R   L   P   N   G   K   L   K   C   D   V   C
541/181                                             571/191
GGC ATG GTT TGC ATT GGG CCC AAT GTG CTT ATG GTA CAT AAA AGG AGT CAC ACT GGT GAA
G   M   V   C   I   G   P   N   V   L   M   V   H   K   R   S   H   T   G   E
601/201                                             631/211
CGC CCC TTC CAC TGT AAC CAG TGT GGA GCT TCT TTT ACT CAG AAG GGC AAC CTT CTG AGA
R   P   F   H   C   N   Q   C   G   A   S   F   T   Q   K   G   N   L   L   R
661/221                                             691/231
CAC ATA AAG TTA CAC TCT GGA GAG AAG CCG TTC AAA TGT CCT TTC TGT AGT CAC GCC TGT
H   I   K   L   H   S   G   E   K   P   F   K   C   P   F   C   S   H   A   C
721/241                                             751/251
AGA AGA AGG GAC GCC CTC ACA GGA TAC CTC AGG ACC CAT TCT GTG GGT AAA CCT CAC AAG
R   R   R   D   A   L   T   G   Y   L   R   T   H   S   V   G   K   P   H   K
781/261                                             811/271
TGC AAC TAC TGT GGA CGA AGC TAC AAG CAG CGC AGT TCA CTG GAG GAG CAC AAG GAA CGC
C   N   Y   C   G   R   S   Y   K   Q   R   S   S   L   E   E   H   K   E   R
841/281                                             871/291
TGC CAC AAC TAT CTC CAG AAT GTC AGC ATG GAG GCT GCT GGG CAG GTC ATG AGT CAC CAT
C   H   N   Y   L   Q   N   V   S   M   E   A   A   G   Q   V   M   S   H   H
901/301                                             931/311
GTA CCT CCT ATG GAA GAT TGT AAG GAA CAA GAG CCT ATT ATG GAC AAC AAT ATT TCT CTG
V   P   P   M   E   D   C   K   E   Q   E   P   I   M   D   N   N   I   S   L
961/321                                             991/331
GTG CCT TTT GAG AGA CCT GCT GTC ATA GAG AAG CTC ACG GGG AAT ATG GGA AAA CGT AAA
V   P   F   E   R   P   A   V   I   E   K   L   T   G   N   M   G   K   R   K
1021/341                                            1051/351
AGC TCC ACT CCA CAA AAG TTT GTG GGG GAA AAG CTC ATG CGA TTC AGC TAC CCA GAT ATT
S   S   T   P   Q   K   F   V   G   E   K   L   M   R   F   S   Y   P   D   I
1081/361                                            1111/371
CAC TTT GAT ATG AAC TTA ACA TAT GAG AAG GAG GCT GAG CTG ATG CAG TCT CAT ATG ATG
H   F   D   M   N   L   T   Y   E   K   E   A   E   L   M   Q   S   H   M   M
1141/381                                            1171/391
GAC CAA GCC ATC AAC AAT GCA ATC ACC TAC CTT GGA GCT GAG GCC CTT CAC CCT CTG ATG
D   Q   A   I   N   N   A   I   T   Y   L   G   A   E   A   L   H   P   L   M
1201/401                                            1231/411
CAG CAC CCG CCA AGC ACA ATC GCT GAA GTG GCC CCA GTT ATA AGC TCA GCT TAT TCT CAG
Q   H   P   P   S   T   I   A   E   V   A   P   V   I   S   S   A   Y   S   Q
```

FIG. 5
(1 of 2)

```
1261/421                                                1291/431
GTC TAT CAT CCA AAT AGG ATA GAA AGA CCC ATT AGC AGG GAA ACT GCT GAT AGT CAT GAA
V   Y   H   P   N   R   I   E   R   P   I   S   R   E   T   A   D   S   H   E
1321/441                                                1351/451
AAC AAC ATG GAT GGC CCC ATC TCT CTC ATC AGA CCA AAG AGT CGA CCC CAG GAA AGA GAG
N   N   M   D   G   P   I   S   L   I   R   P   K   S   R   P   Q   E   R   E
1381/461                                                1411/471
GCC TCT CCC AGC AAT AGC TGC CTG GAT TCC ACT GAC TCA GAA AGC AGC CAT GAT GAC CAC
A   S   P   S   N   S   C   L   D   S   T   D   S   E   S   S   H   D   D   H
1441/481                                                1471/491
CAG TCC TAC CAA GGA CAC CCT GCC TTA AAT CCC AAG AGG AAA CAA AGC CCA GCT TAC ATG
Q   S   Y   Q   G   H   P   A   L   N   P   K   R   K   Q   S   P   A   Y   M
1501/501                                                1531/511
AAG GAG GAT GTC AAA GCT TTG GAT ACT ACC AAG GCT CCT AAG GGC TCT CTG AAG GAC ATC
K   E   D   V   K   A   L   D   T   T   K   A   P   K   G   S   L   K   D   I
1561/521                                                1591/531
TAC AAG GTC TTC AAT GGG GAA GGA GAA CAG ATT AGG GCC TTC AAG TGT GAG CAC TGC CGA
Y   K   V   F   N   G   E   G   E   Q   I   R   A   F   K   C   E   H   C   R
1621/541                                                1651/551
GTC CTT TTC CTA GAC CAT GTC ATG TAC ACC ATT CAC ATG GGT TGC CAT GGC TAC CGG GAC
V   L   F   L   D   H   V   M   Y   T   I   H   M   G   C   H   G   Y   R   D
1681/561                                                1711/571
CCA CTG GAA TGT AAC ATC TGT GGC TAC AGA AGC CAG GAC CGT TAT GAG TTT TCA TCA CAC
P   L   E   C   N   I   C   G   Y   R   S   Q   D   R   Y   E   F   S   S   H
1741/581                                                1771/591
ATT GTT CGA GGG GAG CAC ACA TTC CAC TAG GCC TTT TCA TTC CAA AGG GGA CCC TAT GAA
I   V   R   G   E   H   T   F   H   *   A   F   S   F   Q   R   G   P   Y   E
1801/601                                                1831/611
GTA AAG ACT GCA CAT GAA GAA ATA CTG CAC TTA CAA TCC CAC CTT TCC TCA AAT GTT GTA
V   K   T   A   H   E   E   I   L   H   L   Q   S   H   L   S   S   N   V   V
1861/621                                                1891/631
CCT TTT ATT TTT TTA ATA TAA TAC TGG TGA TAA TCT TAT TTT GTG GAG CAG TGT CAT TTG
P   F   I   F   L   I   *   Y   W   *   *   S   Y   F   V   E   Q   C   H   L
1921/641
CTC TGC T
L   C
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FIG. 5
(2 of 2)

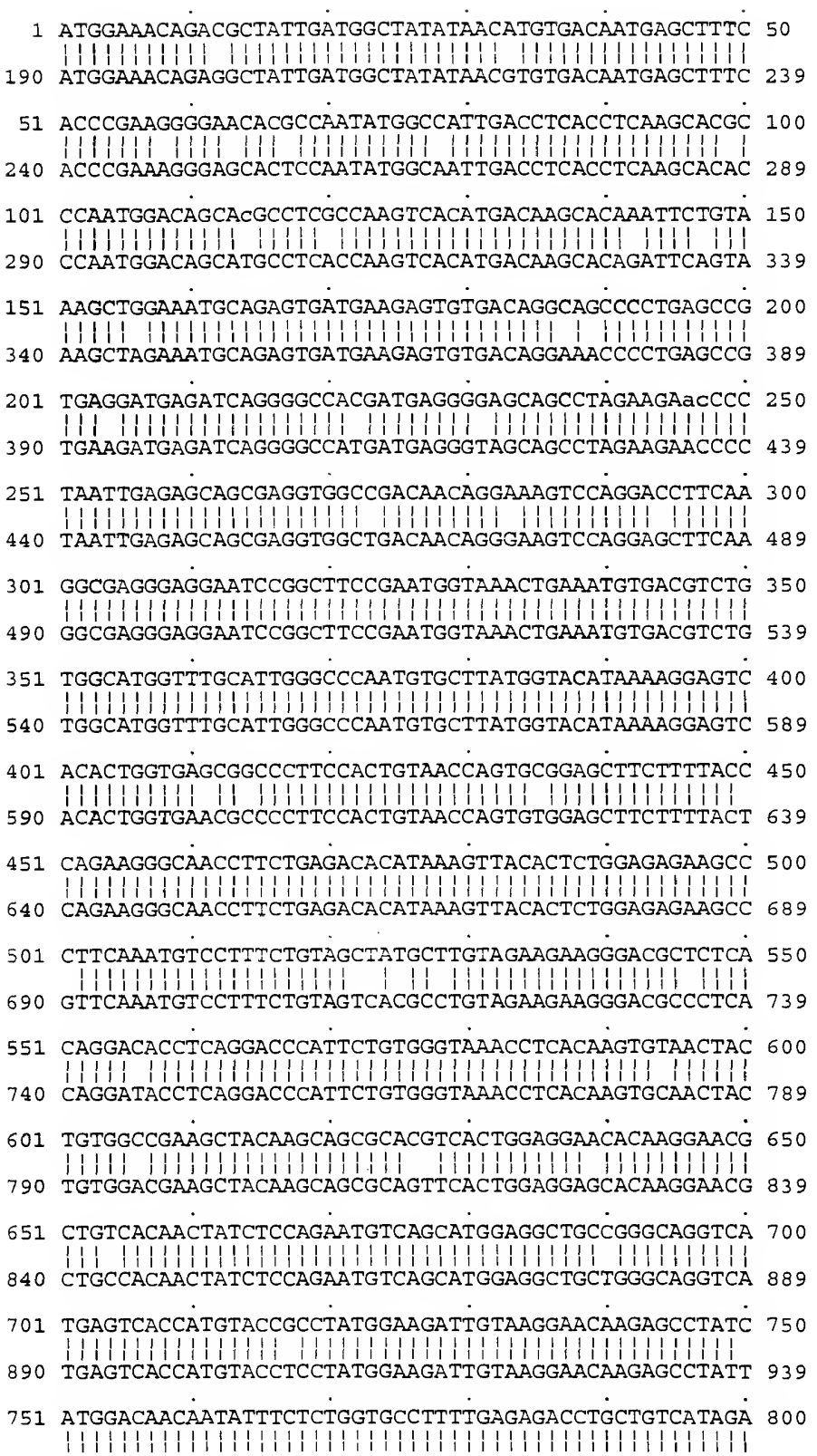
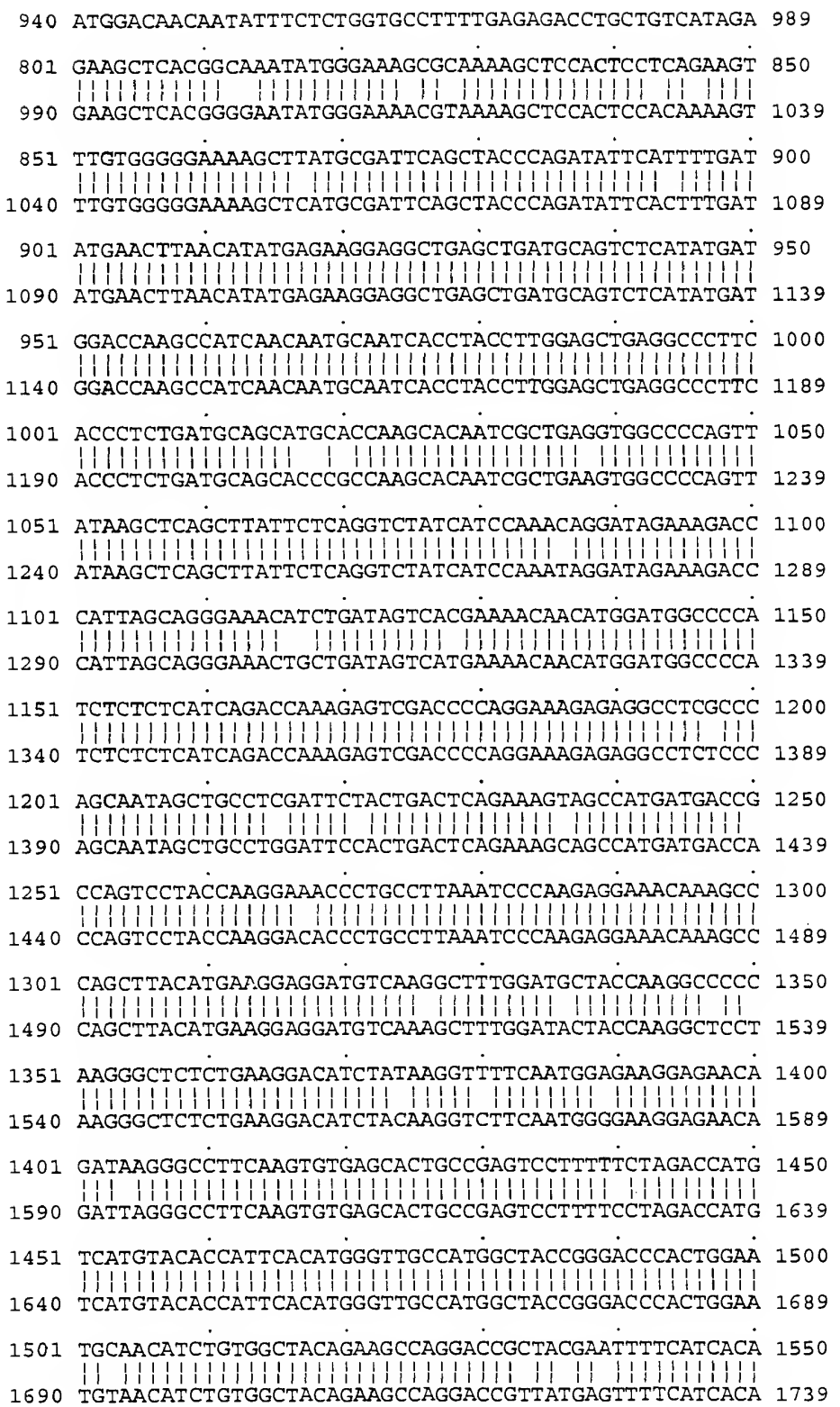

1 ATGGAAACAGACGCTATTGATGGCTATATAACATGTGACAATGAGCTTTC 50
190 ATGGAAACAGAGGCTATTGATGGCTATATAACGTGTGACAATGAGCTTTC 239
51 ACCCGAAGGGGAACACGCCAATATGGCCATTGACCTCACCTCAAGCACGC 100
240 ACCCGAAAGGGAGCACTCCAATATGGCAATTGACCTCACCTCAAGCACAC 289
101 CCAATGGACAGCAcGCCTCGCCAAGTCACATGACAAGCACAAATTCTGTA 150
290 CCAATGGACAGCATGCCTCACCAAGTCACATGACAAGCACAGATTCAGTA 339
151 AAGCTGGAAATGCAGAGTGATGAAGAGTGTGACAGGCAGCCCCTGAGCCG 200
340 AAGCTAGAAATGCAGAGTGATGAAGAGTGTGACAGGAAACCCCTGAGCCG 389
201 TGAGGATGAGATCAGGGGCCACGATGAGGGGAGCAGCCTAGAAGAacCCC 250
390 TGAAGATGAGATCAGGGGCCATGATGAGGGTAGCAGCCTAGAAGAACCCC 439
251 TAATTGAGAGCAGCGAGGTGGCCGACAACAGGAAAGTCCAGGACCTTCAA 300
440 TAATTGAGAGCAGCGAGGTGGCTGACAACAGGGAAGTCCAGGAGCTTCAA 489
301 GGCGAGGGAGGAATCCGGCTTCCGAATGGTAAACTGAAATGTGACGTCTG 350
490 GGCGAGGGAGGAATCCGGCTTCCGAATGGTAAACTGAAATGTGACGTCTG 539
351 TGGCATGGTTTGCATTGGGCCCAATGTGCTTATGGTACATAAAAGGAGTC 400
540 TGGCATGGTTTGCATTGGGCCCAATGTGCTTATGGTACATAAAAGGAGTC 589
401 ACACTGGTGAGCGGCCCTTCCACTGTAACCAGTGCGGAGCTTCTTTTACC 450
590 ACACTGGTGAACGCCCCTTCCACTGTAACCAGTGTGGAGCTTCTTTTACT 639
451 CAGAAGGGCAACCTTCTGAGACACATAAAGTTACACTCTGGAGAGAAGCC 500
640 CAGAAGGGCAACCTTCTGAGACACATAAAGTTACACTCTGGAGAGAAGCC 689
501 CTTCAAATGTCCTTTCTGTAGCTATGCTTGTAGAAGAAGGGACGCTCTCA 550
690 GTTCAAATGTCCTTTCTGTAGTCACGCCTGTAGAAGAAGGGACGCCCTCA 739
551 CAGGACACCTCAGGACCCATTCTGTGGGTAAACCTCACAAGTGTAACTAC 600
740 CAGGATACCTCAGGACCCATTCTGTGGGTAAACCTCACAAGTGCAACTAC 789
601 TGTGGCCGAAGCTACAAGCAGCGCACGTCACTGGAGGAACACAAGGAACG 650
790 TGTGGACGAAGCTACAAGCAGCGCAGTTCACTGGAGGAGCACAAGGAACG 839
651 CTGTCACAACTATCTCCAGAATGTCAGCATGGAGGCTGCCGGGCAGGTCA 700
840 CTGCCACAACTATCTCCAGAATGTCAGCATGGAGGCTGCTGGGCAGGTCA 889
701 TGAGTCACCATGTACCGCCTATGGAAGATTGTAAGGAACAAGAGCCTATC 750
890 TGAGTCACCATGTACCTCCTATGGAAGATTGTAAGGAACAAGAGCCTATT 939
751 ATGGACAACAATATTTCTCTGGTGCCTTTTGAGAGACCTGCTGTCATAGA 800

FIG. 6
(1 of 3)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990 GAAGCTCACGGGGAATATGGGAAAACGTAAAAGCTCCACTCCACAAAAGT 1039
851 TTGTGGGGGAAAAGCTTATGCGATTCAGCTACCCAGATATTCATTTTGAT 900
1040 TTGTGGGGGAAAAGCTCATGCGATTCAGCTACCCAGATATTCACTTTGAT 1089
901 ATGAACTTAACATATGAGAAGGAGGCTGAGCTGATGCAGTCTCATATGAT 950
1090 ATGAACTTAACATATGAGAAGGAGGCTGAGCTGATGCAGTCTCATATGAT 1139
951 GGACCAAGCCATCAACAATGCAATCACCTACCTTGGAGCTGAGGCCCTTC 1000
1140 GGACCAAGCCATCAACAATGCAATCACCTACCTTGGAGCTGAGGCCCTTC 1189
1001 ACCCTCTGATGCAGCATGCACCAAGCACAATCGCTGAGGTGGCCCCAGTT 1050
1190 ACCCTCTGATGCAGCACCCGCCAAGCACAATCGCTGAAGTGGCCCCAGTT 1239
1051 ATAAGCTCAGCTTATTCTCAGGTCTATCATCCAAACAGGATAGAAAGACC 1100
1240 ATAAGCTCAGCTTATTCTCAGGTCTATCATCCAAATAGGATAGAAAGACC 1289
1101 CATTAGCAGGGAAACATCTGATAGTCACGAAAACAACATGGATGGCCCCA 1150
1290 CATTAGCAGGGAAACTGCTGATAGTCATGAAAACAACATGGATGGCCCCA 1339
1151 TCTCTCTCATCAGACCAAAGAGTCGACCCCAGGAAAGAGAGGCCTCGCCC 1200
1340 TCTCTCTCATCAGACCAAAGAGTCGACCCCAGGAAAGAGAGGCCTCTCCC 1389
1201 AGCAATAGCTGCCTCGATTCTACTGACTCAGAAAGTAGCCATGATGACCG 1250
1390 AGCAATAGCTGCCTGGATTCCACTGACTCAGAAAGCAGCCATGATGACCA 1439
1251 CCAGTCCTACCAAGGAAACCCTGCCTTAAATCCCAAGAGGAAACAAAGCC 1300
1440 CCAGTCCTACCAAGGACACCCTGCCTTAAATCCCAAGAGGAAACAAAGCC 1489
1301 CAGCTTACATGAAGGAGGATGTCAAGGCTTTGGATGCTACCAAGGCCCCC 1350
1490 CAGCTTACATGAAGGAGGATGTCAAAGCTTTGGATACTACCAAGGCTCCT 1539
1351 AAGGGCTCTCTGAAGGACATCTATAAGGTTTTCAATGGAGAAGGAGAACA 1400
1540 AAGGGCTCTCTGAAGGACATCTACAAGGTCTTCAATGGGGAAGGAGAACA 1589
1401 GATAAGGGCCTTCAAGTGTGAGCACTGCCGAGTCCTTTTTCTAGACCATG 1450
1590 GATTAGGGCCTTCAAGTGTGAGCACTGCCGAGTCCTTTTCCTAGACCATG 1639
1451 TCATGTACACCATTCACATGGGTTGCCATGGCTACCGGGACCCACTGGAA 1500
1640 TCATGTACACCATTCACATGGGTTGCCATGGCTACCGGGACCCACTGGAA 1689
1501 TGCAACATCTGTGGCTACAGAAGCCAGGACCGCTACGAATTTTCATCACA 1550
1690 TGTAACATCTGTGGCTACAGAAGCCAGGACCGTTATGAGTTTTCATCACA 1739

FIG. 6

(2 of 3)

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1551 CATTGTTGGGGGGCAGCACACATTCCACTAGGCGTTTGCATTCCAAGG 1598
     ||||||| | ||| ||||||||||||||||||| ||| |||||||| |
1740 CATTGTTCGAGGGGAGCACACATTCCACTAGGCCTTTTCATTCCAAAG 1787
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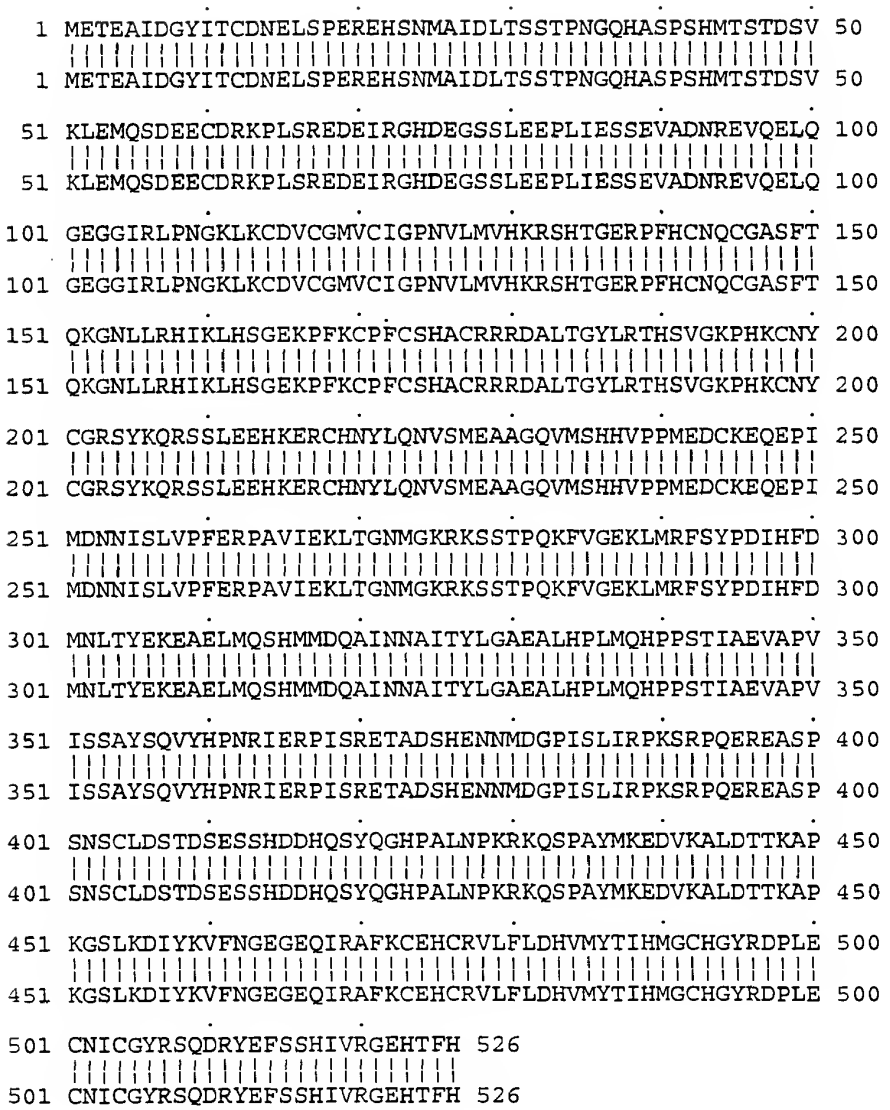
FIG. 6
(3 of 3)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1 METEAIDGYITCDNELSPEREHSNMAIDLTSSTPNGQHASPSHMTSTDSV 50
51 KLEMQSDEECDRKPLSREDEIRGHDEGSSLEEPLIESSEVADNREVQELQ 100
51 KLEMQSDEECDRKPLSREDEIRGHDEGSSLEEPLIESSEVADNREVQELQ 100
101 GEGGIRLPNGKLKCDVCGMVCIGPNVLMVHKRSHTGERPFHCNQCGASFT 150
101 GEGGIRLPNGKLKCDVCGMVCIGPNVLMVHKRSHTGERPFHCNQCGASFT 150
151 QKGNLLRHIKLHSGEKPFKCPFCSHACRRRDALTGYLRTHSVGKPHKCNY 200
151 QKGNLLRHIKLHSGEKPFKCPFCSHACRRRDALTGYLRTHSVGKPHKCNY 200
201 CGRSYKQRSSLEEHKERCHNYLQNVSMEAAGQVMSHHVPPMEDCKEQEPI 250
201 CGRSYKQRSSLEEHKERCHNYLQNVSMEAAGQVMSHHVPPMEDCKEQEPI 250
251 MDNNISLVPFERPAVIEKLTGNMGKRKSSTPQKFVGEKLMRFSYPDIHFD 300
251 MDNNISLVPFERPAVIEKLTGNMGKRKSSTPQKFVGEKLMRFSYPDIHFD 300
301 MNLTYEKEAELMQSHMMDQAINNAITYLGAEALHPLMQHPPSTIAEVAPV 350
301 MNLTYEKEAELMQSHMMDQAINNAITYLGAEALHPLMQHPPSTIAEVAPV 350
351 ISSAYSQVYHPNRIERPISRETADSHENNMDGPISLIRPKSRPQEREASP 400
351 ISSAYSQVYHPNRIERPISRETADSHENNMDGPISLIRPKSRPQEREASP 400
401 SNSCLDSTDSESSHDDHQSYQGHPALNPKRKQSPAYMKEDVKALDTTKAP 450
401 SNSCLDSTDSESSHDDHQSYQGHPALNPKRKQSPAYMKEDVKALDTTKAP 450
451 KGSLKDIYKVFNGEGEQIRAFKCEHCRVLFLDHVMYTIHMGCHGYRDPLE 500
451 KGSLKDIYKVFNGEGEQIRAFKCEHCRVLFLDHVMYTIHMGCHGYRDPLE 500
501 CNICGYRSQDRYEFSSHIVRGEHTFH 526
501 CNICGYRSQDRYEFSSHIVRGEHTFH 526

FIG. 7